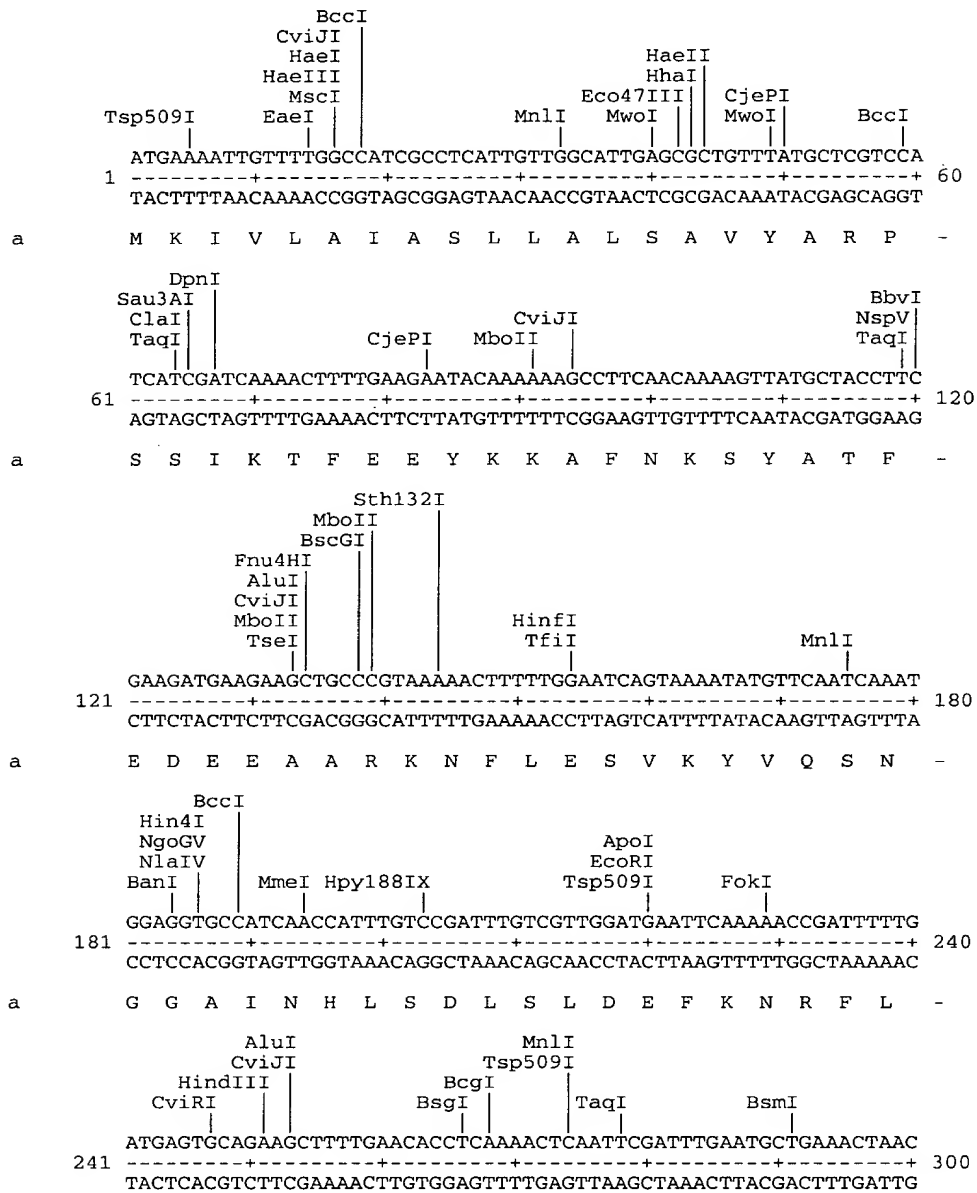




FIGURE 7: DerP1 restriction map of SEQ ID NO. 6.

(Linear) MAP of: Derp1.seq check: 7532 from: 1 to: 963

ID DP11695 standard; RNA; INV; 1099 BP.



a

M S S A E A F E H L K T Q F D L N A E T N -

BpmI PstI BsaXI
CviRI AclI
Cac8I CviJI AluI
SfcI MspAII CviJI
BcgI PvuII ClaI
CjePI MwoI CjePI MaeIII
Tsp45I

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG

301 360

a

A C S I N G N A P A E I D L R Q M R T V -

CviRI MnlI
MslI CviJI DrdII NlaIII
CviJI BsbI
Fnu4HI
TauI

ACTCCCATTCGTATGCAAGGAGGCTGTGGTTCATGTTGGGCTTTCTCTGGTGTGCGCGCA
TGAGGGTAAGCATACGTTCCCTCCGACACCAAGTACAACCCGAAAGAGACCACACGGCGT

361 420

a

T P I R M Q G G C G S C W A F S G V A A -

HinfI AluI CviJI DpnI
TfiI CviJI MwoI TaaI BstYI
Sau3AI AlwI Tsp509I

ACTGAATCAGCTTATTGGGCTTACCGTAATCAATCATGGATCTTGCTGAACAAGAATTA
TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTCTTAAT

421 480

a

T E S A Y L A Y R N Q S L D L A E Q E L -

TaqI BsaAI
FokI
PmlI
BsbI TaaI NlaIII
CjeI MaeII
HphI

GTCGATTGTGCTTCCCAACACGGTTGTTCATGGTGATACCATTCACGTTGATTGAATAC
CAGCTAACACGAAGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG

481 540

a

V D C A S Q H G C H G D T I P R G I E Y -

CjeI MslI
BstXI AluI
MneI CviJI MaeII
ClaI BssSI
TaqI CviRI

ATCCAACATAATGGTGTCTGCTCCAAGAAAGCTACTATCGATACGTTGCACGAGAACATCA
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGCTGCTCTTGTTAGT

541 600

a

I Q H N G V V Q E S Y Y R Y V A R E Q S -

NlaIII CviRI AclI
MaeII ApoI
Tsp509I
CjeI

TGCCGACGACCAATGCACAACGTTTCGGTATCTCAAATATTGCCAAATTTACCCACCA
ACGGCTGCTGGTTTACGTGTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT

601 660

a

C R R P N A Q R F G I S N Y C Q I Y P P -

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AluI
CviJI
CjeI
HindIII
Hpy178III
ApoI
Tsp509I
CviJI
BceI
Eco47III
HaeII
HhaI
RleAI

661 AATGTAACAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720
-----+-----+-----+-----+-----+
TTACATTGTTTTAAGCACTTCGAAACCGAGTTTGGGTGTCGCGATAACGGCAGTAATAA

a N V N K I R E A L A Q T H S A I A V I I -

CviJI
HaeIII
BccI
EaeI
GdiII
SfaNI
BsmI
HgaI
MslI
ThaI

721 GGCATCAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780
-----+-----+-----+-----+-----+
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA

a G I K D L D A F R H Y D G R T I I Q R D -

BstEII
MaeIII
HincII
MaeIII
TaaI
DraIII

781 AATGGTTACCAACCAAACTATCACGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840
-----+-----+-----+-----+-----+
TTACCAATGGTTGGTTTGTAGTGCGACAGTTGTAACAACCAATGTCTATTGCGTGTTCCA

a N G Y Q P N Y H A V N I V G Y S N A Q G -

CjeI
TaaI
BciVI
CjePI
AlwI
RsaI
SunI
DpnI
Sau3AI
TaqI
HgiEII
MunI
Tsp509I
MaeIII
CjePI
HphI
BbvI
TaaI
CjeI

841 GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900
-----+-----+-----+-----+-----+
CAGCTAATAACCTAGCATGCTTTGTCAACCCTATGGTTAACCCACTATTACCAATGCCA

a V D Y W I V R N S W D T N W G D N G Y G -

Fnu4HI
TseI
ClaI
TaqI
Bsp24I
CjePI
CjeI
MboII
NdeI

901 TATTTTGCTGCCAACATCGATTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960
-----+-----+-----+-----+-----+
ATAAAACGACGGTTGTAGCTAAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG

a Y F A A N I D L M M I E E Y P Y V V I L -

TAA
661 --- 963
ATT

FIGURE 8: Sequence of full mutant DerP1 including pre-protein. Active site mutation Cys 132→Ala 132, corresponding to Cys34→Ala34 of the mature protein). Sequence includes coding (listed as SEQ ID NO. [[5]]6) and complementary DNA, and amino acid sequences (listed as SEQ ID NO. [[6]]1).

```
ATGAAAATTGTTTTGGCCATCGCCTCATTGTTGGCATTGAGCGCTGTTTATGCTCGTCCA 60
-----+-----+-----+-----+-----+-----+
TACTTTTAACAAAACCGGTAGCGGAGTAACAACCGTAACTCGCGACAAATACGAGCAGGT
M K I V L A I A S L L A L S A V Y A R P 20

TCATCGATCAAACTTTTGAAGAATACAAAAAGCCTTCAACAAAAGTTATGCTACCTTC 120
-----+-----+-----+-----+-----+-----+
AGTAGCTAGTTTTGAAAACCTTCTTATGTTTTTTCGGAAGTTGTTTTCAATACGATGGAAG
S S I K T F E E Y K K A F N K S Y A T F 40

GAAGATGAAGAAGCTGCCCCGTAAAACTTTTTGGAATCAGTAAATATGTTCAATCAAAT 180
-----+-----+-----+-----+-----+-----+
CTTCTACTTCTTCGACGGGCATTTTTGAAAAACCTTAGTCATTTTATACAAGTTAGTTTA
E D E E A A R K N F L E S V K Y V Q S N 60

GGAGGTGCCATCAACCATTTGTCCGATTTGTCTGTTGGATGAATTCAAAAACCGATTTTTTG 240
-----+-----+-----+-----+-----+-----+
CCTCCACGGTAGTTGGTAAACAGGCTAAACAGCAACCTACTTAAGTTTTTGGCTAAAAAC
G G A I N H L S D L S L D E F K N R F L 80

ATGAGTGCAGAAGCTTTTGAACACCTCAAACTCAATTCGATTTGAATGCTGAACTAAC 300
-----+-----+-----+-----+-----+-----+
TACTCACGTCTTCGAAAACCTTGTGGAGTTTTGAGTTAAGCTAAACTTACGACTTTGATTG
M S A E A F E H L K T Q F D L N A E T N 100

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360
-----+-----+-----+-----+-----+-----+
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
A C S I N G N A P A E I D L R Q M R T V 120

ACTCCCATTTCGTATGCAAGGAGGCTGTGGTTCAGCTTGGGCTTTCTCTGGTGTGCGCA 420
-----+-----+-----+-----+-----+-----+
TGAGGGTAAGCATACGTTCCCTCCGACACCAAGTCGAACCCGAAAGAGACCACAACGGCGT
T P I R M Q G G C G S A W A F S G V A A 140

ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTGGATCTTGCTGAACAAGAATTA 480
-----+-----+-----+-----+-----+-----+
TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
T E S A Y L A Y R N Q S L D L A E Q E L 160
```

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GTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATACCATTCCACGTGGTATTGAATAC 540
-----+-----+-----+-----+-----+-----+-----+
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG
V D C A S Q H G C H G D T I P R G I E Y 180

ATCCAACATAATGGTGTCTGTCCTCAAGAAAGCTACTATCGATACGTTGCACGAGAACAAATCA 600
-----+-----+-----+-----+-----+-----+-----+
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT
I Q H N G V V Q E S Y Y R Y V A R E Q S 200

TGCCGACGACCAAATGCACAACGTTTCGGTATCTCAAACCTATTGCCAAATTTACCCACCA 660
-----+-----+-----+-----+-----+-----+-----+
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT
C R R P N A Q R F G I S N Y C Q I Y P P 220

AATGTAAACAAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720
-----+-----+-----+-----+-----+-----+-----+
TTACATTTGTTTTAAGCACTTCGAAACCGAGTTTGGGTGTCGCGATAACGGCAGTAATAA
N V N K I R E A L A Q T H S A I A V I I 240

GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780
-----+-----+-----+-----+-----+-----+-----+
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA
G I K D L D A F R H Y D G R T I I Q R D 260

AATGGTTACCAACCAAACCTATCACGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840
-----+-----+-----+-----+-----+-----+-----+
TTACCAATGGTTGGTTTGATAGTGCGACAGTTGTAACAACCAATGTCATTGCGTGTTCCA
N G Y Q P N Y H A V N I V G Y S N A Q G 280

GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900
-----+-----+-----+-----+-----+-----+-----+
CAGCTAATAACCTAGCATGCTTTGTCAACCCTATGGTTAACCCCACTATTACCAATGCCA
V D Y W I V R N S W D T N W G D N G Y G 300

TATTTTGCTGCCAACATCGATTTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960
-----+-----+-----+-----+-----+-----+-----+
ATAAAACGACGGTTGTAGCTAAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG
Y F A A N I D L M M I E E Y P Y V V I L 320

TAA

ATT

FIGURE 9: Sequence of full mutant DerP1 including pre-protein containing a deletion at the propeptide cleavage site (NAET). Sequence includes coding (listed as SEQ ID NO. [[1]]2) and complementary DNA, and amino acid sequences (listed as SEQ ID NO. 2).

```
ATGAAAATTGTTTTGGCCATCGCCTCATTGTTGGCATTGAGCGCTGTTTATGCTCGTCCA 60
-----+-----+-----+-----+-----+-----+
TACTTTTAACAAAACCGGTAGCGGAGTAACAACCGTAACCTCGCGACAAATACGAGCAGGT
M K I V L A I A S L L A L S A V Y A R P 20

TCATCGATCAAACTTTTGAAGAATACAAAAAGCCTTCAACAAAAGTTATGCTACCTTC 120
-----+-----+-----+-----+-----+-----+
AGTAGCTAGTTTTGAAAACCTTCTTATGTTTTTTTCGGAAGTTGTTTTCAATACGATGGAAG
S S I K T F E E Y K K A F N K S Y A T F 40

GAAGATGAAGAAGCTGCCCCGTAAAACTTTTTGGAATCAGTAAAAATATGTTCAATCAAAAT 180
-----+-----+-----+-----+-----+-----+
CTTCTACTTCTTCGACGGGCATTTTTGAAAAACCTTAGTCATTTTATACAAGTTAGTTTA
E D E E A A R K N F L E S V K Y V Q S N 60

GGAGGTGCCATCAACCATTTGTCCGATTTGTCGTTGGATGAATTCAAAAACCGATTTTTTG 240
-----+-----+-----+-----+-----+-----+
CCTCCACGGTAGTTGGTAAACAGGCTAAACAGCAACCTACTTAAGTTTTTGGCTAAAAAC
G G A I N H L S D L S L D E F K N R F L 80

ATGAGTGCAGAAGCTTTTGAACACCTCAAACTCAATTCGATTTG AAC 300
-----+-----+-----+-----+-----+-----+
TACTCACGTCTTCGAAAACCTGTGGAGTTTGTAGTTAAGCTAAAC TTG
M S A E A F E H L K T Q F D L N 100

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360
-----+-----+-----+-----+-----+-----+
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
A C S I N G N A P A E I D L R Q M R T V 120

ACTCCCATTTCGTATGCAAGGAGGCTGTGGTTCATGTTGGGCTTTCTCTGGTGTTGCCGCA 420
-----+-----+-----+-----+-----+-----+
TGAGGGTAAGCATACGTTCTCCGACACCAAGTACAACCCGAAAGAGACCACAACGGCGT
T P I R M Q G G C G S C W A F S G V A A 140

ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTGGATCTTGCTGAACAAGAATTA 480
-----+-----+-----+-----+-----+-----+
TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
T E S A Y L A Y R N Q S L D L A E Q E L 160
```

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GTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATACCATTCCACGTGGTATTGAATAC 540
-----+-----+-----+-----+-----+-----+-----+
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG
V D C A S Q H G C H G D T I P R G I E Y 180

ATCCAACATAATGGTGTGCTCCAAGAAAGCTACTATCGATACGTTGCACGAGAACAATCA 600
-----+-----+-----+-----+-----+-----+-----+
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT
I Q H N G V V Q E S Y Y R Y V A R E Q S 200

TGCCGACGACCAAATGCACAACGTTTCGGTATCTCAAACCTATTGCCAAATTTACCCACCA 660
-----+-----+-----+-----+-----+-----+-----+
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT
C R R P N A Q R F G I S N Y C Q I Y P P 220

AATGTAAACAAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720
-----+-----+-----+-----+-----+-----+-----+
TTACATTTGTTTAAAGCACTTCGAAACCGAGTTTGGGTGTGCGGATAACGGCAGTAATAA
N V N K I R E A L A Q T H S A I A V I I 240

GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780
-----+-----+-----+-----+-----+-----+-----+
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA
G I K D L D A F R H Y D G R T I I Q R D 260

AATGGTTACCAACCAAACTATGCTGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840
-----+-----+-----+-----+-----+-----+-----+
TTACCAATGGTTGGTTTGATAGTGCGACAGTTGTAACAACCAATGTCATTGCGTGTTCCA
N G Y Q P N Y A A V N I V G Y S N A Q G 280

GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900
-----+-----+-----+-----+-----+-----+-----+
CAGCTAATAACCTAGCATGCTTTGTCAACCCCTATGGTTAACCCCACTATTACCAATGCCA
V D Y W I V R N S W D T N W G D N G Y G 300

TATTTTGCTGCCAACATCGATTTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960
-----+-----+-----+-----+-----+-----+-----+
ATAAAACGACGGTTGTAGCTAAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG
Y F A A N I D L M M I E E Y P Y V V I L 320

TAA

ATT

FIGURE 10: Sequence of full mutant DerP1 including pre-protein. Active site mutation His 268 → Ala 268, corresponding to His170→Ala170 of the mature protein). Sequence includes coding (listed as SEQ ID NO. [[3]]8) and complementary DNA, and amino acid sequences (listed as SEQ ID NO. [[4]]3).

```
ATGAAAATTGTTTTGGCCATCGCCTCATTGTTGGCATTGAGCGCTGTTTATGCTCGTCCA 60
-----+-----+-----+-----+-----+-----+
TACTTTTAACAAAACCGGTAGCGGAGTAACAACCGTAACTCGCGACAAATACGAGCAGGT
M K I V L A I A S L L A L S A V Y A R P 20

TCATCGATCAAAACTTTTGAAGAATACAAAAAGCCTTCAACAAAAGTTATGCTACCTTC 120
-----+-----+-----+-----+-----+-----+
AGTAGCTAGTTTTGAAAACCTTCTTATGTTTTTCGGAAGTTGTTTTCAATACGATGGAAG
S S I K T F E E Y K K A F N K S Y A T F 40

GAAGATGAAGAAGCTGCCCCGTAAAAACTTTTTGGAATCAGTAAATATGTTCAATCAAAT 180
-----+-----+-----+-----+-----+-----+
CTTCTACTTCTTCGACGGGCATTTTTGAAAACCTTAGTCATTTTATACAAGTTAGTTTA
E D E E A A R K N F L E S V K Y V Q S N 60

GGAGGTGCCATCAACCATTTGTCCGATTTGTCGTTGGATGAATTCAAAAACCGATTTTTTG 240
-----+-----+-----+-----+-----+-----+
CCTCCACGGTAGTTGGTAAACAGGCTAAACAGCAACCTACTTAAGTTTTTGGCTAAAAAC
G G A I N H L S D L S L D E F K N R F L 80

ATGAGTGCAGAAGCTTTTGAACACCTCAAAACTCAATTCGATTTGAATGCTGAAACTAAC 300
-----+-----+-----+-----+-----+-----+
TACTCACGTCTTCGAAAACCTTGTTGGAGTTTTGAGTTAAGCTAAACTTACGACTTTGATTG
M S A E A F E H L K T Q F D L N A E T N 100

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360
-----+-----+-----+-----+-----+-----+
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
A C S I N G N A P A E I D L R Q M R T V 120

ACTCCCATTTCGTATGCAAGGAGGCTGTGGTTCATGTTGGGCTTTCTCTGGTGTGCGCA 420
-----+-----+-----+-----+-----+-----+
TGAGGGTAAGCATACGTTCCCTCCGACACCAAGTACAACCCGAAAGAGACCACAACGGCGT
T P I R M Q G G C G S C W A F S G V A A 140

ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTGGATCTTGCTGAACAAGAATTA 480
-----+-----+-----+-----+-----+-----+
TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
T E S A Y L A Y R N Q S L D L A E Q E L 160
```


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GTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATACCATTCCACGTGGTATTGAATAC 540
-----+-----+-----+-----+-----+-----+-----+
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG
V D C A S Q H G C H G D T I P R G I E Y 180

ATCCAACATAATGGTGTGCTCCAAGAAAGCTACTATCGATACGTTGCACGAGAACAATCA 600
-----+-----+-----+-----+-----+-----+-----+
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT
I Q H N G V V Q E S Y Y R Y V A R E Q S 200

TGCCGACGACCAAATGCACAACGTTTCGGTATCTCAAACCTATTGCCAAATTTACCCACCA 660
-----+-----+-----+-----+-----+-----+-----+
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT
C R R P N A Q R F G I S N Y C Q I Y P P 220

AATGTAAACAAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720
-----+-----+-----+-----+-----+-----+-----+
TTACATTTGTTTAAAGCACTTCGAAACCGAGTTTGGGTGTGCGGATAACGGCAGTAATAA
N V N K I R E A L A Q T H S A I A V I I 240

GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780
-----+-----+-----+-----+-----+-----+-----+
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA
G I K D L D A F R H Y D G R T I I Q R D 260

AATGGTTACCAACCAAACCTATGCTGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840
-----+-----+-----+-----+-----+-----+-----+
TTACCAATGGTTGGTTTGATACGACGACAGTTGTAACAACCAATGTCATTGCGTGTTCCA
N G Y Q P N Y A A V N I V G Y S N A Q G 280

GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900
-----+-----+-----+-----+-----+-----+-----+
CAGCTAATAACCTAGCATGCTTTGTCAACCCCTATGGTTAACCCCACTATTACCAATGCCA
V D Y W I V R N S W D T N W G D N G Y G 300

TATTTTGCTGCCAACATCGATTTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960
-----+-----+-----+-----+-----+-----+-----+
ATAAAACGACGGTTGTAGCTAAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG
Y F A A N I D L M M I E E Y P Y V V I L 320

TAA

ATT

FIGURE 11: Amino acid sequence (SEQ ID NO: [[7]]4) for the mutant DerP1 as encoded by pNIV4842, and shown in figure 5.

1 MLLVNQSHQG FNKEHTSKMV SAIVLYVLLA AAAHSAFAAD PRPSSIKTFE
51 EYKKAFNKS Y ATFEDDEEAAR KNFLESVKYV QSNNGGAINHL SDLSLDEFKN
101 RFLMSAEAFE HLKTQFDLNA CSINGNAPAE IDLRQMRTVT PIRMQGGCGS
151 CWA FSGVAAT ESAYLAYRNQ SLDLAEQELV DCASQHGCHG DTIPRGIEYI
201 QHNGVVQESY YRYVAREQSC RRPNAQRFGI SNYCQIYPPN ANKIREALAQ
251 THSAIAVIIG IKDLDAFRHY DGRTIIQRDN GYQPNYHAVN IVGYSNAQGV
301 DYWIVRNSWD TNWGDNGYGY FAANIDLMMI EEYPYVVIL*



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FIGURE 12: Amino acid sequence (SEQ ID NO: [[8]]5) for the mutant DerP1 as encoded by pNIV4843, and shown in figure 6.

1 MLLVNQSHQG FNKEHTSKMV SAIVLYVLLA AAAHSAFAAD PRPSSIKTFE
51 EYKKA FNKSY ATFEDEEAAR KNFLESVKYV QSNGGAINHL SDLSLDEFKN
101 RFLMSAEAFE HLKTQFDLNA ETNACSINGN APAEIDLRQM RTVTPIRMQG
151 GCGSAWAFSG VAATESAYLA YRNQSLDLAE QELVDCASQH GCHGDTIPRG
201 IEYIQHNGVV QESYYRYVAR EQSCRRPNAQ RFGISNYCQI YPPNANKIRE
251 ALAQTHSAIA VIIGIKDLDA FRHYDGRTII QRDNGYQPNY HAVNIVGYSN
301 AQGVVDYWIVR NSWDTNWGDN GYGYFAANID LMMIEEYPYV VIL*